

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/633,200

DATE: 10/23/2001
TIME: 15:17:10

Input Set : N:\Crif3\RULE60\09633200.txt
Output Set: N:\CRF3\10232001\I633200.raw

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:

- 6 (i) APPLICANT: KIEFER, MICHAEL C.
7 BARR, PHILIP J.
- 9 (ii) TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA
10 ENCODING THE PROTEINS AND METHODS OF USE THEREOF
- 12 (iii) NUMBER OF SEQUENCES: 22
- 14 (iv) CORRESPONDENCE ADDRESS:
15 (A) ADDRESSEE: MORRISON & FOERSTER
16 (B) STREET: 755 Page Mill Road
17 (C) CITY: Palo Alto
18 (D) STATE: California
19 (E) COUNTRY: USA
20 (F) ZIP: 94304-1018
- 22 (v) COMPUTER READABLE FORM:
23 (A) MEDIUM TYPE: Floppy disk
24 (B) COMPUTER: IBM PC compatible
25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
26 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- 28 (vi) CURRENT APPLICATION DATA:
29 (A) APPLICATION NUMBER: US/09/633,200
30 (B) FILING DATE: 07-Aug-2000
31 (C) CLASSIFICATION:
- 33 (vii) PRIOR APPLICATION DATA:
34 (A) APPLICATION NUMBER: US 08/320,157
35 (B) FILING DATE: 07-OCT-1994
- 38 (viii) ATTORNEY/AGENT INFORMATION:
39 (A) NAME: LEHNHARDT, SUSAN K.
40 (B) REGISTRATION NUMBER: 33,943
41 (C) REFERENCE/DOCKET NUMBER: 23647-20007.20
- 43 (ix) TELECOMMUNICATION INFORMATION:
44 (A) TELEPHONE: (415) 813-5600
45 (B) TELEFAX: (415) 494-0792
46 (C) TELEX: 706141
- 49 (2) INFORMATION FOR SEQ ID NO: 1:
51 (i) SEQUENCE CHARACTERISTICS:
52 (A) LENGTH: 8 amino acids
53 (B) TYPE: amino acid
54 (C) STRANDEDNESS: single
55 (D) TOPOLOGY: linear
- 61 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
63 Asp Trp Gly Arg Val Val Ala Ile
64 1 5
- 66 (2) INFORMATION FOR SEQ ID NO: 2:
68 (i) SEQUENCE CHARACTERISTICS:
69 (A) LENGTH: 36 base pairs
70 (B) TYPE: nucleic acid

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10/23/01

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71      (C) STRANDEDNESS: single
72      (D) TOPOLOGY: linear
76      (ix) FEATURE:
77          (A) NAME/KEY: misc_difference
78          (B) LOCATION: replace(23, "")
79          (D) OTHER INFORMATION: /note= "This position is inosine."
81      (ix) FEATURE:
82          (A) NAME/KEY: misc_difference
83          (B) LOCATION: replace(27, "")
84          (D) OTHER INFORMATION: /note= "This position is inosine."
87      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2: 36
89 AGATCTGAAT TCAACTTGGG GGNCAGNAGT NGTNGC
91 (2) INFORMATION FOR SEQ ID NO: 3:
93      (i) SEQUENCE CHARACTERISTICS:
94          (A) LENGTH: 11 amino acids
95          (B) TYPE: amino acid
96          (C) STRANDEDNESS: single
97          (D) TOPOLOGY: linear
103      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
105      Asp Trp Gly Gly Gln Glu Asn Asp Gln Ile Trp
106          1          5          10
108 (2) INFORMATION FOR SEQ ID NO: 4:
110      (i) SEQUENCE CHARACTERISTICS:
111          (A) LENGTH: 29 base pairs
112          (B) TYPE: nucleic acid
113          (C) STRANDEDNESS: single
114          (D) TOPOLOGY: linear
118      (ix) FEATURE:
119          (A) NAME/KEY: misc_difference
120          (B) LOCATION: replace(6, "")
121          (D) OTHER INFORMATION: /note= "This position is inosine."
123      (ix) FEATURE:
124          (A) NAME/KEY: misc_difference
125          (B) LOCATION: replace(9, "")
126          (D) OTHER INFORMATION: /note= "This position is inosine."
129      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4: 29
131 AGGGTNGGNG GNACNAGAGA CATCTAGGT
133 (2) INFORMATION FOR SEQ ID NO: 5:
135      (i) SEQUENCE CHARACTERISTICS:
136          (A) LENGTH: 41 base pairs
137          (B) TYPE: nucleic acid
138          (C) STRANDEDNESS: single
139          (D) TOPOLOGY: linear
143      (ix) FEATURE:
144          (A) NAME/KEY: misc_difference
145          (B) LOCATION: replace(19, "")
146          (D) OTHER INFORMATION: /note= "This position is inosine."
148      (ix) FEATURE:
149          (A) NAME/KEY: misc_difference

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150      (B) LOCATION: replace(22, "")
151      (D) OTHER INFORMATION: /note= "This position is inosine."
154      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
156 AGATCTAAGC TTGTCCCAAC CNCNTGNTC CTGAGATCC A      41
158 (2) INFORMATION FOR SEQ ID NO: 6:
160      (i) SEQUENCE CHARACTERISTICS:
161          (A) LENGTH: 2094 base pairs
162          (B) TYPE: nucleic acid
163          (C) STRANDEDNESS: single
164          (D) TOPOLOGY: linear
168      (ix) FEATURE:
169          (A) NAME/KEY: CDS
170          (B) LOCATION: 201..833
173      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
175 GAGGATCTAC AGGGGACAAG TAAAGGCTAC ATCCAGATGC CGGGAATGCA CTGACGCCCCA      60
177 TTCTTGAAAA CTGGGCTCCC ACTCAGCCCC TGGGAGCAGC AGCCGCCAGC CCCTCGGACC      120
179 TCCATCTCCA CCCTGCTGAG CCACCCGGGT TGGGCCAGGA TCCCGGCAGG CTGATCCCGT      180
181 CCTCCACTGA GACCTGAAAA ATG GCT TCG GGG CAA GGC CCA GGT CCT CCC      230
182      Met Ala Ser Gly Gln Gly Pro Gly Pro Pro
183      1 5 10
185 AGG CAG GAG TGC GGA GAG CCT GCC CTG CCC TCT GCT TCT GAG GAG CAG      278
186 Arg Gln Glu Cys Gly Glu Pro Ala Leu Pro Ser Ala Ser Glu Glu Gln
187      15 20 25
189 GTA GCC CAG GAC ACA GAG GAG GTT TTC CGC AGC TAC GTT TTT TAC CGC      326
190 Val Ala Gln Asp Thr Glu Glu Val Phe Arg Ser Tyr Val Phe Tyr Arg
191      30 35 40
193 CAT CAG CAG GAA CAG GAG GCT GAA GGG GTG GCT GCC CCT GCC GAC CCA      374
194 His Gln Gln Glu Gln Glu Ala Glu Gly Val Ala Ala Pro Ala Asp Pro
195      45 50 55
197 GAG ATG GTC ACC TTA CCT CTG CAA CCT AGC AGC ACC ATG GGG CAG GTG      422
198 Glu Met Val Thr Leu Pro Leu Gln Pro Ser Ser Thr Met Gly Gln Val
199      60 65 70
201 GGA CGG CAG CTC GCC ATC ATC GGG GAC GAC ATC AAC CGA CGC TAT GAC      470
202 Gly Arg Gln Leu Ala Ile Ile Gly Asp Asp Ile Asn Arg Arg Tyr Asp
203 75 80 85 90
205 TCA GAG TTC CAG ACC ATG TTG CAG CAC CTG CAG CCC ACG GCA GAG AAT      518
206 Ser Glu Phe Gln Thr Met Leu Gln His Leu Gln Pro Thr Ala Glu Asn
207      95 100 105
209 GCC TAT GAG TAC TTC ACC AAG ATT GCC ACC AGC CTG TTT GAG AGT GGC      566
210 Ala Tyr Glu Tyr Phe Thr Lys Ile Ala Thr Ser Leu Phe Glu Ser Gly
211      110 115 120
213 ATC AAT TGG GGC CGT GTG GTG GCT CTT CTG GGC TTC GGC TAC CGT CTG      614
214 Ile Asn Trp Gly Arg Val Val Ala Leu Leu Gly Phe Gly Tyr Arg Leu
215      125 130 135
217 GCC CTA CAC GTC TAC CAG CAT GGC CTG ACT GGC TTC CTA GGC CAG GTG      662
218 Ala Leu His Val Tyr Gln His Gly Leu Thr Gly Phe Leu Gly Gln Val
219      140 145 150
221 ACC CGC TTC GTG GTC GAC TTC ATG CTG CAT CAC TGC ATT GCC CGG TGG      710
222 Thr Arg Phe Val Val Asp Phe Met Leu His His Cys Ile Ala Arg Trp

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223 155          160          165          170
225 ATT GCA CAG AGG GGT GGC TGG GTG GCA GCC CTG AAC TTG GGC AAT GGT      758
226 Ile Ala Gln Arg Gly Gly Trp Val Ala Ala Leu Asn Leu Gly Asn Gly
227          175          180          185
229 CCC ATC CTG AAC GTG CTG GTG GTT CTG GGT GTG GTT CTG TTG GGC CAG      806
230 Pro Ile Leu Asn Val Leu Val Val Leu Gly Val Val Leu Leu Gly Gln
231          190          195          200
233 TTT GTG GTA CGA AGA TTC TTC AAA TCA TGA CTCCCAA GGGTGCCTT      853
234 Phe Val Val Arg Arg Phe Phe Lys Ser
235          205          210
237 TGGGTCCCGG TTCAGACCCC TGCCTGGACT TAAGCGAAGT CTTTGCCTTC TCTGTTCCCT      913
239 TGCAGGGTCC CCCCTCAAGA GTACAGAAGC TTTAGCAAGT GTGCACTCCA GCTTCGGAGG      973
241 CCCTGCGTGG GGGCCAGTCA GGCTGCAGAG GCACCTCAAC ATTGCATGGT GCTAGTGCCC      1033
243 TCTCTCTGGG CCCAGGGCTG TGGCCGTCTC CTCCCTCAGC TCTCTGGGAC CTCCTTAGCC      1093
245 CTGTCTGCTA GGCGCTGGGG AGACTGATAA CTTGGGGAGG CAAGAGACTG GGAGCCACTT      1153
247 CTCCCCAGAA AGTGTTTAAG GGTTTTAGCT TTTTATAATA CCCTTGTGAG AGCCCATTCC      1213
249 CACCATTCTA CCTGAGGCCA GGACGTCTGG GGTGTGGGGA TTGGTGGGTC TATGTTCCCC      1273
251 AGGATTGAGC TATTCTGGAA GATCAGCACC CTAAGAGATG GGAAGTAGG CTGAGCCTGG      1333
253 TCCTGGCCGT CCCTAAGCAT GTGTCCCAGG AGCAGGACCT ACTAGGAGAG GGGGGCCAAG      1393
255 GTCCTGCTCA ACTCTACCCC TGCTCCCATC CCTCCCTCCG GCCATACTGC CTTTGCAGTT      1453
257 GGAATCTCAG GGATTCTGGG CTTGGGGTGT GGGGTGGGGT GGAGTCGCAG ACCAGAGCTG      1513
259 TCTGAATCA CGTGTCAAGG GCCTCCAAGC CTGCTCCCA AGGTCTCTCT AGTTCTCTCC      1573
261 CTTCTCTCTC CTTTATAGAC ACTTGCTCCC AATCCATTCA CTACAGGTGA AGGCTCTCAC      1633
263 CCATCCCTGG GGGCCTTGGG TGAGTGGCCT GCTAAGGCTC CTCCTTGCCC AGACTACAGG      1693
265 GCTTAGGACT TGGTTTGTTA TATCAGGGAA AAGGAGTAGG GAGTTCATCT GGAGGGTTCT      1753
267 AAGTGGGAGA AGGACTATCA ACACCACTAG GAATCCCAGA GGTGGATCCT CCCTCATGGC      1813
269 TCTGGCACAG TGTAATCCAG GGGGTGTAGAT GGGGGAAGTG TGAATACTTG AACTCTGTTT      1873
271 CCCCACCTTC CATGCTCCTC ACCTGTCTAG GTCTCCTCAG GGTGGGGGGT GACAGTGCCT      1933
273 TCTCTATTGG CACAGCCTAG GGTCTTGGGG GTCAGGGGGG AGAAGTTCTT GATTACGCCA      1993
275 AATGCAGGGA GGGGAGGCAG ATGGAGCCCA TAGGCCACCC CCTATCCTCT GAGTGTGTTG      2053
277 AAATAAACTG TGCAATCCCC TCAAAAAAAA AACGGAGATC C      2094
280 (2) INFORMATION FOR SEQ ID NO: 7:
282 (i) SEQUENCE CHARACTERISTICS:
283 (A) LENGTH: 211 amino acids
284 (B) TYPE: amino acid
285 (D) TOPOLOGY: linear
287 (ii) MOLECULE TYPE: protein
289 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
291 Met Ala Ser Gly Gln Gly Pro Gly Pro Pro Arg Gln Glu Cys Gly Glu
292 1 5 10 15
294 Pro Ala Leu Pro Ser Ala Ser Glu Glu Gln Val Ala Gln Asp Thr Glu
295 20 25 30
297 Glu Val Phe Arg Ser Tyr Val Phe Tyr Arg His Gln Gln Glu Gln Glu
298 35 40 45
300 Ala Glu Gly Val Ala Ala Pro Ala Asp Pro Glu Met Val Thr Leu Pro
301 50 55 60
303 Leu Gln Pro Ser Ser Thr Met Gly Gln Val Gly Arg Gln Leu Ala Ile
304 65 70 75 80
306 Ile Gly Asp Asp Ile Asn Arg Arg Tyr Asp Ser Glu Phe Gln Thr Met

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307          85          90          95
309 Leu Gln His Leu Gln Pro Thr Ala Glu Asn Ala Tyr Glu Tyr Phe Thr
310          100          105          110
312 Lys Ile Ala Thr Ser Leu Phe Glu Ser Gly Ile Asn Trp Gly Arg Val
313          115          120          125
315 Val Ala Leu Leu Gly Phe Gly Tyr Arg Leu Ala Leu His Val Tyr Gln
316          130          135          140
318 His Gly Leu Thr Gly Phe Leu Gly Gln Val Thr Arg Phe Val Val Asp
319 145          150          155          160
321 Phe Met Leu His His Cys Ile Ala Arg Trp Ile Ala Gln Arg Gly Gly
322          165          170          175
324 Trp Val Ala Ala Leu Asn Leu Gly Asn Gly Pro Ile Leu Asn Val Leu
325          180          185          190
327 Val Val Leu Gly Val Val Leu Leu Gly Gln Phe Val Val Arg Arg Phe
328          195          200          205
330 Phe Lys Ser
331          210

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333 (2) INFORMATION FOR SEQ ID NO: 8:

335 (i) SEQUENCE CHARACTERISTICS:

336 (A) LENGTH: 1287 base pairs

337 (B) TYPE: nucleic acid

338 (C) STRANDEDNESS: single

339 (D) TOPOLOGY: linear

343 (ix) FEATURE:

344 (A) NAME/KEY: CDS

345 (B) LOCATION: 544..1176

348 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

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350 TTTTAATATA AATTAATGTG CTCTATTAT AGAGACAATA CATGAAATAT ACTTAATAAA      60
352 AATTCAAATG TTATAGAACT GAAAAAGATG AAAAGTAAAA ACAACCTATT CCCCAGAGGT      120
354 AGCCACTGTC CATAGTTTCT ATTTTAGATT CTTTCCTTTA TACAAGATTA TTATAGCTTC      180
356 TATTTTTTGG TGTATGAACT GTAGTCCTAG AGGATTTTAT TAGTTATGAG TTCTATAACT      240
358 AAGATCCATC ATCTTAGTTG CTAAGAACGT AGATACTGAG AACATCATTT AAAAAACAT      300
360 TTTTGGCTGG CACCTCATGA TCACTGGAGT CTCGCGGGTC CCTCAGGCTG CACAGGGACA      360
362 AGTAAAGGCT ACATCCAGAT GCTGGGAATG CACTGACGCC CATTCTGGA AACTGGGCTC      420
364 CCACTCAGCC CCTGGGAGCA GCAGCCGCCA GCCCCTCGGG ACCTCCATCT CCACCCTGCT      480
366 GAGCCACCCG GGTTGGGCCA GGATCCCGGC AGGCTGATCC CGTCCTCCAC TGAGACCTGA      540
368 AAA ATG GCT TCG GGG CAA GGC CCA GGT CCT CCC AGG CAG GAG TGC GGA      588
369 Met Ala Ser Gly Gln Gly Pro Gly Pro Pro Arg Gln Glu Cys Gly
W--> 370          215          220          225
372 GAG CCT GCC CTG CCC TCT GCT TCT GAG GAG CAG GTA GCC CAG GAC ACA      636
373 Glu Pro Ala Leu Pro Ser Ala Ser Glu Glu Gln Val Ala Gln Asp Thr
W--> 374          230          235          240
376 GAG GAG GTT TTC CGC AGC TAC GTT TTT TAC CAC CAT CAG CAG GAA CAG      684
377 Glu Glu Val Phe Arg Ser Tyr Val Phe Tyr His His Gln Gln Glu Gln
W--> 378          245          250          255
380 GAG GCT GAA GGG GCG GCT GCC CCT GCC GAC CCA GAG ATG GTC ACC TTA      732
381 Glu Ala Glu Gly Ala Ala Ala Pro Ala Asp Pro Glu Met Val Thr Leu
W--> 382          260          265          270
384 CCT CTG CAA CCT AGC AGC ACC ATG GGG CAG GTG GGA CGG CAG CTC GCC      780

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VERIFICATION SUMMARY

DATE: 10/23/2001

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Input Set : N:\Crf3\RULE60\09633200.txt

Output Set: N:\CRF3\10232001\I633200.raw

L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:370 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:8
L:374 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:8
L:378 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:8
L:382 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:8
L:386 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:8
L:390 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:8
L:394 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:8
L:398 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:8
L:402 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:8
L:406 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:8
L:410 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:8
L:414 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:8
L:418 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:8
L:422 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:8
L:1110 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:20
L:1114 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:20
L:1118 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:20
L:1122 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:20
L:1126 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:20
L:1130 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:20
L:1136 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:20